

Additional file 1 (Tables and Figures)

Table S1. Characterization of upland cotton (*Gossypium hirsutum*) MAPKKK family.

Gene name	Gene symbol	Protein Length(aa)	MW(kDa)	pI	Chr	Chr location	subcellular location
<i>GhRAF1</i>	Ghir_A01G013020	790	86.94	5.71	A01	59116528-59124508	nucleus
<i>GhRAF2</i>	Ghir_A01G016390	640	73.17	7.46	A01	106268030-106276569	mitochondria
<i>GhRAF3</i>	Ghir_A02G000450	339	37.98	7.48	A02	265264-268155	cytoplasm
<i>GhRAF4</i>	Ghir_A02G000730	472	53.59	6.65	A02	533011-536829	nucleus
<i>GhRAF5</i>	Ghir_A02G003480	383	42.49	9.52	A02	3913633-3915990	cytoplasm
<i>GhRAF6</i>	Ghir_A02G005560	737	81.69	7.5	A02	7937650-7943308	nucleus
<i>GhRAF7</i>	Ghir_A02G005570	740	82.04	7.1	A02	7967940-7973147	nucleus
<i>GhRAF8</i>	Ghir_A02G019080	531	59.81	9.08	A02	107728162-107734200	cytoplasm
<i>GhRAF9</i>	Ghir_A03G011560	429	48.44	4.72	A03	66726431-66731117	nucleus
<i>GhRAF10</i>	Ghir_A04G007330	851	94.44	6.72	A04	55875639-55885335	chloroplast
<i>GhRAF11</i>	Ghir_A04G013720	560	63.32	6.7	A04	82511312-82523191	cytoplasm
<i>GhRAF12</i>	Ghir_A05G000660	1101	122.21	6.02	A05	791306-798656	nucleus
<i>GhRAF13</i>	Ghir_A05G004450	931	103.68	5.64	A05	4095618-4103212	nucleus
<i>GhRAF14</i>	Ghir_A05G006850	419	46.76	5.87	A05	6210586-6215373	cytoplasm
<i>GhRAF15</i>	Ghir_A05G018630	504	57.03	5.11	A05	17620458-17627531	cytoplasm
<i>GhRAF16</i>	Ghir_A05G036930	352	39.79	5.67	A05	97148360-97152224	cytoplasm
<i>GhRAF17</i>	Ghir_A05G037260	374	41.97	6.36	A05	98076719-98080529	nucleus
<i>GhRAF18</i>	Ghir_A06G003070	915	102.20	5.06	A06	3871954-3879898	nucleus
<i>GhRAF19</i>	Ghir_A06G005200	1361	147.82	6.54	A06	8680343-8685948	nucleus
<i>GhRAF20</i>	Ghir_A06G016490	371	42.45	5.05	A06	114049596-114052061	mitochondria
<i>GhRAF21</i>	Ghir_A07G000080	415	46.36	9.3	A07	122914-127571	cytoplasm
<i>GhRAF22</i>	Ghir_A07G002310	844	94.54	5.41	A07	2497285-2504622	cytoplasm
<i>GhRAF23</i>	Ghir_A07G023620	379	42.39	5	A07	95826552-95830147	nucleus
<i>GhRAF24</i>	Ghir_A07G024120	354	40.03	7.82	A07	96546518-96550072	cytoplasm
<i>GhRAF25</i>	Ghir_A08G007020	1110	122.58	6.85	A08	11163822-11175803	mitochondria
<i>GhRAF26</i>	Ghir_A08G009370	1136	125.95	9.42	A08	36606576-36615782	nucleus
<i>GhRAF27</i>	Ghir_A09G003240	351	39.65	5.78	A09	10448608-10451805	cytoplasm
<i>GhRAF28</i>	Ghir_A09G005960	1035	113.38	5.58	A09	45765254-45780842	nucleus
<i>GhRAF29</i>	Ghir_A09G007360	765	84.97	9.43	A09	54426475-54431583	nucleus
<i>GhRAF30</i>	Ghir_A09G014590	846	94.01	7.02	A09	69970458-69980083	chloroplast
<i>GhRAF31</i>	Ghir_A09G022480	470	53.03	6.3	A09	78659520-78665922	mitochondria
<i>GhRAF32</i>	Ghir_A09G022610	355	39.85	8.8	A09	78818941-78822312	cytoplasm
<i>GhRAF33</i>	Ghir_A09G023270	391	43.58	7.66	A09	79321195-79325067	cytoplasm
<i>GhRAF34</i>	Ghir_A09G024870	777	86.08	7.31	A09	80703148-80707529	nucleus
<i>GhRAF35</i>	Ghir_A10G000530	374	42.65	6.06	A10	359133-362546	mitochondria
<i>GhRAF36</i>	Ghir_A10G014920	472	53.49	9.29	A10	79999093-80009164	chloroplast

<i>GhRAF37</i>	Ghir_A10G017650	815	90.15	5.22	A10	98138758-98144602	plastid
<i>GhRAF38</i>	Ghir_A10G017660	775	85.74	7.85	A10	98138949-98144056	nucleus
<i>GhRAF39</i>	Ghir_A11G007400	383	42.65	9.55	A11	6471350-6476392	cytoplasm
<i>GhRAF40</i>	Ghir_A11G018110	576	65.33	7.83	A11	23594659-23601101	cytoplasm
<i>GhRAF41</i>	Ghir_A12G000340	390	43.49	8.55	A12	498790-502564	cytoplasm
<i>GhRAF42</i>	Ghir_A12G017420	437	49.15	5.65	A12	92993297-92998342	cytoplasm
<i>GhRAF43</i>	Ghir_A12G028160	1005	109.59	5.11	A12	106836116-106845511	chloroplast
<i>GhRAF44</i>	Ghir_A12G028660	405	44.83	8.75	A12	107354905-107359160	nucleus
<i>GhRAF45</i>	Ghir_A13G007800	422	47.24	6.43	A13	22199989-22209556	nucleus
<i>GhRAF46</i>	Ghir_D01G000200	552	62.23	6.47	D01	119887-126036	cytoplasm
<i>GhRAF47</i>	Ghir_D01G014020	859	94.98	6.58	D01	33463668-33473973	nucleus
<i>GhRAF48</i>	Ghir_D01G017900	640	73.22	9.08	D01	54254478-54262863	mitochondria
<i>GhRAF49</i>	Ghir_D02G000450	353	39.42	7.86	D02	292116-295007	cytoplasm
<i>GhRAF50</i>	Ghir_D02G000700	479	54.34	8.52	D02	557041-561510	nucleus
<i>GhRAF51</i>	Ghir_D02G003900	421	47.12	7.26	D02	4871769-4874033	vacuole
<i>GhRAF52</i>	Ghir_D02G005920	612	67.27	9.13	D02	7896079-7899981	nucleus
<i>GhRAF53</i>	Ghir_D02G013070	430	48.50	6.05	D02	43746961-43751699	nucleus
<i>GhRAF54</i>	Ghir_D03G000490	571	64.31	7.63	D03	287684-293745	cytoplasm
<i>GhRAF55</i>	Ghir_D04G005790	374	41.93	6.36	D04	9363047-9371442	nucleus
<i>GhRAF56</i>	Ghir_D04G006140	352	39.80	6.27	D04	9990673-9994944	cytoplasm
<i>GhRAF57</i>	Ghir_D04G011410	769	85.44	6.03	D04	36701936-36715894	chloroplast
<i>GhRAF58</i>	Ghir_D04G018140	581	65.69	5.68	D04	53642245-53651176	cytoplasm
<i>GhRAF59</i>	Ghir_D05G004560	931	103.38	7.9	D05	3654314-3661796	nucleus
<i>GhRAF60</i>	Ghir_D05G018650	546	61.82	7.59	D05	16164014-16171000	cytoplasm
<i>GhRAF61</i>	Ghir_D06G003070	915	102.18	9.17	D06	3677514-3685966	nucleus
<i>GhRAF62</i>	Ghir_D06G017360	371	42.43	8.11	D06	57749167-57752516	mitochondria
<i>GhRAF63</i>	Ghir_D07G000100	415	46.33	4.96	D07	179515-186775	chloroplast
<i>GhRAF64</i>	Ghir_D07G002320	937	104.13	8.16	D07	2398608-2406880	cytoplasm
<i>GhRAF65</i>	Ghir_D07G023720	407	45.62	9.43	D07	57351655-57355299	nucleus
<i>GhRAF66</i>	Ghir_D07G024190	354	39.98	7.02	D07	57953528-57957106	cytoplasm
<i>GhRAF67</i>	Ghir_D08G007100	1110	122.75	6.08	D08	9538439-9550399	mitochondria
<i>GhRAF68</i>	Ghir_D08G009250	1137	126.20	8.2	D08	19075396-19083848	nucleus
<i>GhRAF69</i>	Ghir_D09G003170	368	41.74	9.61	D09	9674313-9676427	cytoplasm
<i>GhRAF70</i>	Ghir_D09G005530	1038	113.70	7.76	D09	25995770-26013030	chloroplast
<i>GhRAF71</i>	Ghir_D09G007100	766	85.43	9.5	D09	31322296-31328509	nucleus
<i>GhRAF72</i>	Ghir_D09G021710	511	58.31	8.45	D09	49737805-49743942	plastid
<i>GhRAF73</i>	Ghir_D09G021860	355	39.85	8.05	D09	49864023-49867444	cytoplasm
<i>GhRAF74</i>	Ghir_D09G022500	391	43.62	5.05	D09	50337160-50340960	cytoplasm
<i>GhRAF75</i>	Ghir_D09G024040	782	86.48	5.3	D09	51636834-51641319	nucleus
<i>GhRAF76</i>	Ghir_D10G001280	374	42.58	9.49	D10	1044184-1047688	mitochondria
<i>GhRAF77</i>	Ghir_D10G012570	472	53.39	6.59	D10	20394725-20405455	chloroplast
<i>GhRAF78</i>	Ghir_D10G015940	407	45.59	6.12	D10	34491476-34496357	nucleus
<i>GhRAF79</i>	Ghir_D10G027360	822	91.39	6.52	D10	42627-48353	nucleus
<i>GhRAF80</i>	Ghir_D10G027370	822	91.39	7.85	D10	42627-48353	nucleus

<i>GhRAF81</i>	Ghir_D11G007370	377	42.05	8.15	D11	5956229-5961305	cytoplasm
<i>GhRAF82</i>	Ghir_D11G013250	391	43.65	9.12	D11	12324700-12328019	nucleus
<i>GhRAF83</i>	Ghir_D11G018170	575	65.08	6.55	D11	19660407-19666208	cytoplasm
<i>GhRAF84</i>	Ghir_D12G000320	390	43.51	4.76	D12	496884-500310	cytoplasm
<i>GhRAF85</i>	Ghir_D12G017630	407	45.66	6.51	D12	50376204-50380659	nucleus
<i>GhRAF86</i>	Ghir_D12G028810	395	44.04	6.92	D12	62344984-62348539	cytoplasm
<i>GhRAF87</i>	Ghir_D13G008130	422	47.36	5.13	D13	14566968-14572225	nucleus
<i>GhMEKK1</i>	Ghir_A01G007310	437	48.73	4.4	A01	12214003-12215349	chloroplast
<i>GhMEKK2</i>	Ghir_A01G001550	1392	153.45	6.38	A01	1347205-1364027	nucleus
<i>GhMEKK3</i>	Ghir_A02G007890	576	63.86	7.86	A02	14863551-14868958	nucleus
<i>GhMEKK4</i>	Ghir_A02G017190	338	37.24	4.8	A02	105635187-105636628	nucleus
<i>GhMEKK5</i>	Ghir_A03G003570	483	54.23	7.04	A03	5378191-5379713	chloroplast
<i>GhMEKK6</i>	Ghir_A05G017620	451	50.22	8.12	A05	16817349-16819236	chloroplast
<i>GhMEKK7</i>	Ghir_A05G023670	590	65.81	7.33	A05	23521490-23527510	mitochondria
<i>GhMEKK8</i>	Ghir_A05G039730	661	71.49	7.83	A05	104396747-104402568	nucleus
<i>GhMEKK9</i>	Ghir_A08G019150	898	96.61	5.83	A08	113804134-113811609	nucleus
<i>GhMEKK10</i>	Ghir_A08G021040	510	57.38	4.66	A08	116673745-116675288	chloroplast
<i>GhMEKK11</i>	Ghir_A09G006310	696	77.07	8.21	A09	48820595-48825206	nucleus
<i>GhMEKK12</i>	Ghir_A10G000750	446	49.88	5.16	A10	542297-544223	chloroplast
<i>GhMEKK13</i>	Ghir_A10G008980	336	37.06	8.89	A10	17413794-17415339	cytoplasm
<i>GhMEKK14</i>	Ghir_A10G009080	609	67.15	5.67	A10	17850579-17854710	chloroplast
<i>GhMEKK15</i>	Ghir_A11G005180	711	78.83	8.93	A11	4446012-4450377	nucleus
<i>GhMEKK16</i>	Ghir_A11G035820	359	40.06	7.85	A11	74237-75959	nucleus
<i>GhMEKK17</i>	Ghir_A11G028650	649	71.28	6.18	A11	110953343-110957688	chloroplast
<i>GhMEKK18</i>	Ghir_A12G000100	659	71.27	9.09	A12	128695-134251	nucleus
<i>GhMEKK19</i>	Ghir_A12G007320	724	79.50	8.34	A12	20022401-20027163	chloroplast
<i>GhMEKK20</i>	Ghir_A12G014480	1419	156.93	6.58	A12	85092129-85106151	nucleus
<i>GhMEKK21</i>	Ghir_A13G024620	480	53.88	4.87	A13	108139019-108140767	nucleus
<i>GhMEKK22</i>	Ghir_D01G001550	1390	153.24	6.42	D01	1117035-1129976	nucleus
<i>GhMEKK23</i>	Ghir_D01G007620	437	48.70	4.4	D01	10460363-10461748	chloroplast
<i>GhMEKK24</i>	Ghir_D02G008300	589	65.29	6.21	D02	13393209-13401017	nucleus
<i>GhMEKK25</i>	Ghir_D02G019480	1433	157.75	6.19	D02	64489810-64506546	nucleus
<i>GhMEKK26</i>	Ghir_D03G002430	338	37.27	4.74	D03	2289862-2291287	nucleus
<i>GhMEKK27</i>	Ghir_D03G015380	466	52.13	7.57	D03	47788539-47791494	chloroplast
<i>GhMEKK28</i>	Ghir_D04G003320	492	54.23	9.47	D04	4494122-4499940	mitochondria
<i>GhMEKK29</i>	Ghir_D05G010730	519	58.18	5.12	D05	9039986-9043494	nucleus
<i>GhMEKK31</i>	Ghir_D05G017600	328	36.08	5.65	D05	15286900-15287915	chloroplast
<i>GhMEKK32</i>	Ghir_D05G023540	590	65.77	5.8	D05	21265802-21271793	mitochondria
<i>GhMEKK33</i>	Ghir_D08G020070	886	95.34	4.71	D08	60648887-60653844	nucleus
<i>GhMEKK34</i>	Ghir_D08G021840	485	54.48	9.29	D08	63216185-63217671	chloroplast
<i>GhMEKK35</i>	Ghir_D09G004580	896	96.72	7.83	D09	17634778-17642198	nucleus
<i>GhMEKK36</i>	Ghir_D09G005940	666	73.65	5.52	D09	27714016-27718642	nucleus
<i>GhMEKK37</i>	Ghir_D10G001500	445	49.28	8.89	D10	1232613-1234017	chloroplast
<i>GhMEKK38</i>	Ghir_D10G010170	613	67.53	6.02	D10	12704209-12708378	chloroplast

<i>GhMEKK39</i>	Ghir_D10G010300	336	37.02	8.25	D10	12944719-12946243	cytoplasm
<i>GhMEKK39</i>	Ghir_D11G005120	711	78.85	8.82	D11	4146812-4151046	nucleus
<i>GhMEKK40</i>	Ghir_D11G020530	359	39.96	6.6	D11	24796013-24797663	nucleus
<i>GhMEKK41</i>	Ghir_D11G028840	663	72.81	6.63	D11	61257989-61262800	chloroplast
<i>GhMEKK42</i>	Ghir_D12G000070	657	71.09	6	D12	118968-123487	nucleus
<i>GhMEKK43</i>	Ghir_D12G007230	724	79.39	8.15	D12	13666895-13671597	chloroplast
<i>GhMEKK44</i>	Ghir_D12G009430	350	39.04	8.37	D12	30737030-30738538	nucleus
<i>GhMEKK45</i>	Ghir_D12G014650	1419	156.77	5.04	D12	45189485-45203561	nucleus
<i>GhMEKK46</i>	Ghir_D13G025390	400	44.60	5.14	D13	63120547-63122405	cytoplasm
<i>GhZIK1</i>	Ghir_A01G007760	294	33.51	4.76	A01	12963498-12965306	nucleus
<i>GhZIK2</i>	Ghir_A02G003230	295	83.12	5.06	A02	3711890-3715525	nucleus
<i>GhZIK3</i>	Ghir_A02G010480	593	68.47	5.54	A02	44849057-44852765	chloroplast
<i>GhZIK4</i>	Ghir_A05G039820	734	68.02	5.63	A05	104503240-104507236	nucleus
<i>GhZIK5</i>	Ghir_A07G006240	643	68.75	8.56	A07	7493603-7497360	nucleus
<i>GhZIK6</i>	Ghir_A08G013280	584	75.45	8.81	A08	95860535-95864059	nucleus
<i>GhZIK7</i>	Ghir_A09G025930	607	72.14	4.79	A09	81675593-81680150	nucleus
<i>GhZIK8</i>	Ghir_A10G015190	300	67.70	4.64	A10	83054890-83059051	nucleus
<i>GhZIK9</i>	Ghir_A11G023700	593	72.43	9.68	A11	71611997-71615920	nucleus
<i>GhZIK10</i>	Ghir_A11G027620	606	65.84	8.11	A11	108571185-108575022	nucleus
<i>GhZIK11</i>	Ghir_A12G025200	610	68.38	6.97	A12	104071155-104075057	nucleus
<i>GhZIK12</i>	Ghir_A13G024870	611	67.42	7.87	A13	108274667-108278662	nucleus
<i>GhZIK13</i>	Ghir_D01G008110	667	33.70	8.33	D01	11151704-11153578	nucleus
<i>GhZIK14</i>	Ghir_D02G003610	639	82.81	6.13	D02	4677447-4681187	nucleus
<i>GhZIK15</i>	Ghir_D04G003230	593	67.82	7.85	D04	4404068-4408048	nucleus
<i>GhZIK16</i>	Ghir_D07G006240	643	68.65	5.83	D07	6781781-6785762	nucleus
<i>GhZIK17</i>	Ghir_D08G014030	573	75.63	6.66	D08	48402157-48405717	nucleus
<i>GhZIK18</i>	Ghir_D09G025080	607	69.97	5.13	D09	52454940-52459320	nucleus
<i>GhZIK19</i>	Ghir_D10G012370	593	67.73	4.85	D10	19337073-19341117	nucleus
<i>GhZIK20</i>	Ghir_D11G024040	734	72.10	5.65	D11	43762327-43766202	nucleus
<i>GhZIK21</i>	Ghir_D11G027780	609	67.05a	5.79	D11	59353199-59356901	nucleus
<i>GhZIK22</i>	Ghir_D12G025200	609	68.57	7.66	D12	59149045-59153596	nucleus
<i>GhZIK23</i>	Ghir_D13G014800	668	34.31	5.99	D13	48319020-48320442	nucleus
<i>GhZIK24</i>	Ghir_D13G025640	621	67.44	4.8	D13	63270786-63274742	nucleus

Note: The DNA and protein sequences of GhMAPKKs can be found in cotton (*G. hirsutum*) genome database (<https://www.cottongen.org>).

Table S2. Orthologous MAPKKK gene pairs of *Gossypium hirsutum*, *G. arboreum*, and *G. raimondii*.

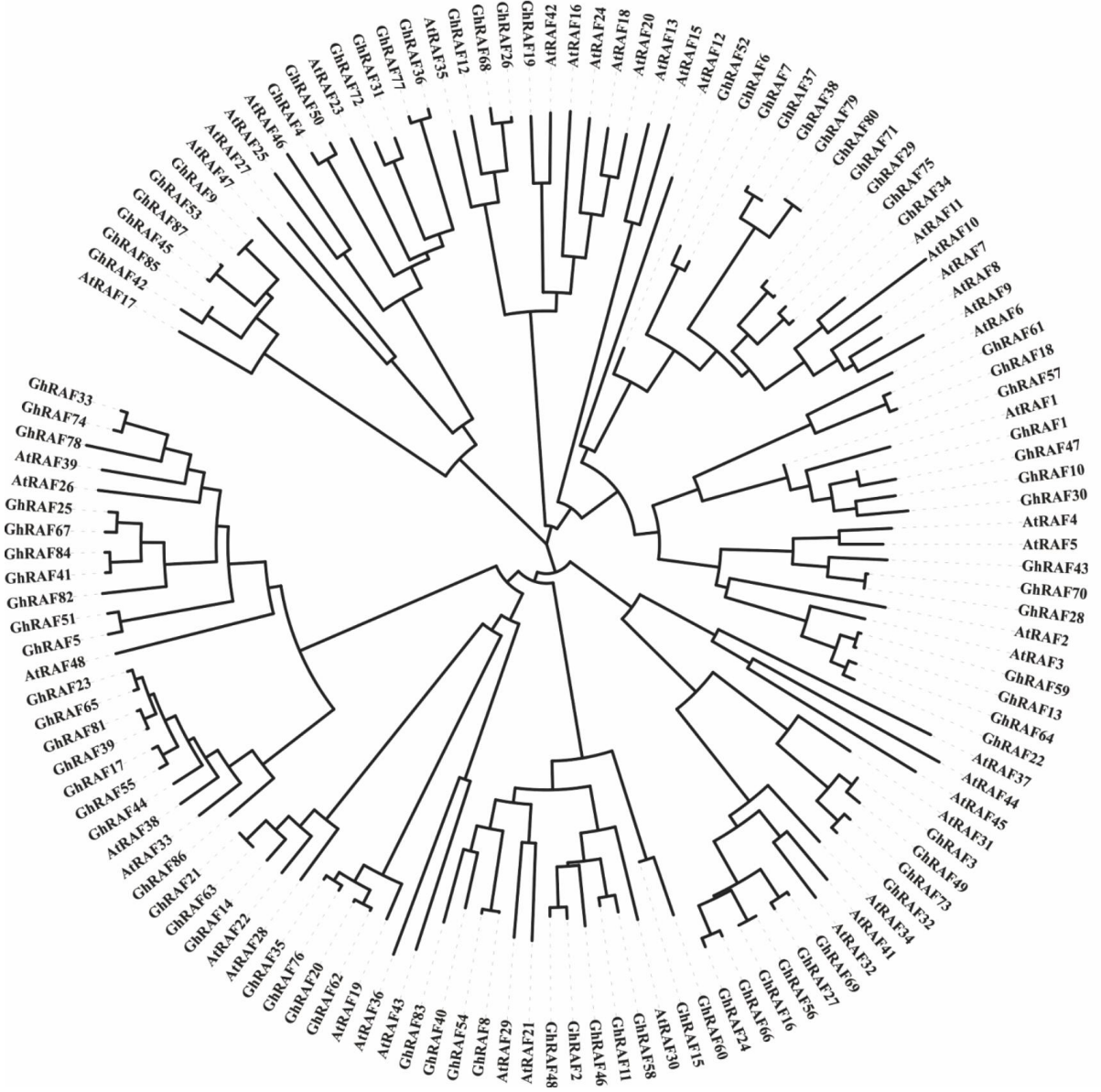
Genes of At subgenome	Orthologous genes in G. arboreum	Genes of Dt subgenome	Orthologous genes of G. raimondii
<i>GhMEKK1</i>	Ga01G0882.1	<i>GhMEKK22</i>	Gorai.002G016000.1
<i>GhMEKK2</i>	Ga01G0174.1	<i>GhMEKK23</i>	Gorai.002G091000.1
<i>GhMEKK3</i>	Ga03G0881.1	<i>GhMEKK24</i>	Gorai.005G091700.1
<i>GhMEKK4</i>	Ga02G0227.1	<i>GhMEKK25</i>	Gorai.005G210100.1
<i>GhMEKK5</i>	Ga01G2525.1	<i>GhMEKK26</i>	Gorai.003G025400.1
<i>GhMEKK6</i>	Ga05G1835.1	<i>GhMEKK27</i>	Gorai.003G146500.1
<i>GhMEKK7</i>	Ga05G2467.1	<i>GhMEKK28</i>	Gorai.012G034500.1
<i>GhMEKK8</i>	Ga04G1803.1	<i>GhMEKK29</i>	Gorai.009G111600.1
<i>GhMEKK9</i>	Ga08G2155.1	<i>GhMEKK31</i>	Gorai.009G242600.1
<i>GhMEKK10</i>	Ga08G2357.1	<i>GhMEKK32</i>	Gorai.004G213200.1
<i>GhMEKK11</i>	Ga09G0760.1	<i>GhMEKK33</i>	Gorai.004G232400.1
<i>GhMEKK12</i>	Ga10G2971.1	<i>GhMEKK34</i>	Gorai.006G049500.1
<i>GhMEKK13</i>	Ga10G2072.1	<i>GhMEKK35</i>	Gorai.006G052900.1
<i>GhMEKK14</i>	Ga10G2060.1	<i>GhMEKK36</i>	Gorai.011G012900.1
<i>GhMEKK15</i>	Ga11G3597.1	<i>GhMEKK37</i>	Gorai.011G104700.1
<i>GhMEKK16</i>	Ga11G1935.1	<i>GhMEKK38</i>	Gorai.011G106000.1
<i>GhMEKK17</i>	Ga11G0898.1	<i>GhMEKK39</i>	Gorai.007G053300.1
<i>GhMEKK18</i>	Ga12G2908.1	<i>GhMEKK40</i>	Gorai.007G213900.1
<i>GhMEKK19</i>	Ga12G2339.1	<i>GhMEKK41</i>	Gorai.007G296700.1
<i>GhMEKK20</i>	Ga12G1545.1	<i>GhMEKK42</i>	Gorai.008G000500.1
<i>GhMEKK21</i>	Ga13G2820.1	<i>GhMEKK43</i>	Gorai.008G073600.1
<i>GhRAF1</i>	Ga01G1576.1	<i>GhMEKK44</i>	Gorai.008G077000.1
<i>GhRAF2</i>	Ga02G1149.1	<i>GhMEKK45</i>	Gorai.008G149400.1
<i>GhRAF3</i>	Ga03G0041.1	<i>GhMEKK46</i>	Gorai.013G269600.1
<i>GhRAF4</i>	Ga03G0070.1	<i>GhRAF46</i>	Gorai.002G002100.1
<i>GhRAF5</i>	Ga03G0390.1	<i>GhRAF47</i>	Gorai.002G159900.1
<i>GhRAF6</i>	Ga03G0610.1	<i>GhRAF48</i>	Gorai.002G201200.1
<i>GhRAF7</i>	Ga03G0611.1	<i>GhRAF49</i>	Gorai.005G004900.1
<i>GhRAF8</i>	Ga02G0049.1	<i>GhRAF50</i>	Gorai.005G007700.1
<i>GhRAF9</i>	Ga03G1413.1	<i>GhRAF51</i>	Gorai.005G044700.1
<i>GhRAF10</i>	Ga04G0943.1	<i>GhRAF52</i>	Gorai.005G067300.1
<i>GhRAF11</i>	Ga04G0244.1	<i>GhRAF53</i>	Gorai.005G142900.1
<i>GhRAF12</i>	Ga05G0062.1	<i>GhRAF54</i>	Gorai.003G005100.1
<i>GhRAF13</i>	Ga05G0456.1	<i>GhRAF55</i>	Gorai.001G261300.1
<i>GhRAF14</i>	Ga05G0706.1	<i>GhRAF56</i>	Gorai.012G064800.1
<i>GhRAF15</i>	Ga05G1937.1	<i>GhRAF57</i>	Gorai.009G408200.1
<i>GhRAF16</i>	Ga04G1468.1	<i>GhRAF58</i>	Gorai.012G157000.1
<i>GhRAF17</i>	Ga04G1511.1	<i>GhRAF59</i>	Gorai.009G045200.1
<i>GhRAF18</i>	Ga14G0424.1	<i>GhRAF60</i>	Gorai.009G190600.1
<i>GhRAF19</i>	Ga06G0496.1	<i>GhRAF61</i>	Gorai.010G033900.1

<i>GhRAF20</i>	Ga06G1869.1	<i>GhRAF62</i>	Gorai.010G185600.1
<i>GhRAF21</i>	Ga07G0011.1	<i>GhRAF63</i>	Gorai.001G001200.1
<i>GhRAF22</i>	Ga07G0240.1	<i>GhRAF64</i>	Gorai.001G022800.1
<i>GhRAF23</i>	Ga07G2547.1	<i>GhRAF66</i>	Gorai.001G266100.1
<i>GhRAF24</i>	Ga07G2599.1	<i>GhRAF67</i>	Gorai.004G077800.1
<i>GhRAF25</i>	Ga08G0757.1	<i>GhRAF68</i>	Gorai.004G101000.1
<i>GhRAF26</i>	Ga08G1003.1	<i>GhRAF69</i>	Gorai.006G034500.1
<i>GhRAF27</i>	Ga14G1817.1	<i>GhRAF70</i>	Gorai.006G056600.1
<i>GhRAF28</i>	Ga09G0686.1	<i>GhRAF71</i>	Gorai.006G080100.1
<i>GhRAF29</i>	Ga14G0576.1	<i>GhRAF72</i>	Gorai.006G233100.1
<i>GhRAF30</i>	Ga09G1563.1	<i>GhRAF73</i>	Gorai.006G234800.1
<i>GhRAF31</i>	Ga09G2426.1	<i>GhRAF74</i>	Gorai.006G241500.1
<i>GhRAF32</i>	Ga09G2438.1	<i>GhRAF75</i>	Gorai.006G258400.1
<i>GhRAF33</i>	Ga09G2365.1	<i>GhRAF76</i>	Gorai.011G010500.1
<i>GhRAF34</i>	Ga09G2670.1	<i>GhRAF77</i>	Gorai.011G131000.1
<i>GhRAF35</i>	Ga10G2994.1	<i>GhRAF78</i>	Gorai.011G167400.1
<i>GhRAF36</i>	Ga10G1766.1	<i>GhRAF79</i>	Gorai.011G200300.1
<i>GhRAF38</i>	Ga10G1015.1	<i>GhRAF81</i>	Gorai.007G076700.1
<i>GhRAF39</i>	Ga11G3372.1	<i>GhRAF82</i>	Gorai.007G139200.1
<i>GhRAF40</i>	Ga11G2193.1	<i>GhRAF83</i>	Gorai.007G190200.1
<i>GhRAF41</i>	Ga12G2886.1	<i>GhRAF84</i>	Gorai.008G003000.1
<i>GhRAF42</i>	Ga12G1203.1	<i>GhRAF85</i>	Gorai.008G179300.1
<i>GhRAF43</i>	Ga12G0091.1	<i>GhRAF86</i>	Gorai.008G294700.1
<i>GhRAF44</i>	Ga12G0039.1	<i>GhRAF87</i>	Gorai.013G089100.1
<i>GhRAF45</i>	Ga13G0934.1	<i>GhZIK13</i>	Gorai.002G096100.1
<i>GhZIK1</i>	Ga01G0928.1	<i>GhZIK14</i>	Gorai.005G042400.1
<i>GhZIK2</i>	Ga03G0365.1	<i>GhZIK15</i>	Gorai.012G033500.1
<i>GhZIK3</i>	Ga01G1804.1	<i>GhZIK16</i>	Gorai.001G064400.1
<i>GhZIK4</i>	Ga04G1748.1	<i>GhZIK17</i>	Gorai.004G150400.1
<i>GhZIK5</i>	Ga07G0665.1	<i>GhZIK18</i>	Gorai.006G269500.1
<i>GhZIK6</i>	Ga08G1482.1	<i>GhZIK19</i>	Gorai.011G128900.1
<i>GhZIK7</i>	Ga09G2783.1	<i>GhZIK20</i>	Gorai.003G069600.1
<i>GhZIK8</i>	Ga10G1803.1	<i>GhZIK21</i>	Gorai.007G285300.1
<i>GhZIK9</i>	Ga14G2590.1	<i>GhZIK22</i>	Gorai.008G257300.1
<i>GhZIK10</i>	Ga11G0996.1	<i>GhZIK23</i>	Gorai.013G156000.1
<i>GhZIK11</i>	Ga12G0406.1	<i>GhZIK24</i>	Gorai.013G272100.1
<i>GhZIK12</i>	Ga14G0657.1		

Table S3. Primers used in vector construction and quantitative RT-PCR analysis.

Gene	Primer
<i>GhRAF4-F</i>	GGAATTCCAAGGACAGCCATTCAGACCC
<i>GhRAF4-R</i>	GGGTACCCTGGACGTGCTAATTTGGCCT
<i>GhMEKK12-F</i>	GGAATTCCTGCCGTTAAGTCCTCTGAGC
<i>GhMEKK12-R</i>	GGGTACCCATGTCAGCTGGGAACCCCTG
<i>GhMEKK10-RT-F</i>	GCTTGGCGATCCACCAATCAGA
<i>GhMEKK10-RT-R</i>	CGCCGCCGAGGATTCATTCTTA
<i>GhMEKK12-RT-F</i>	GAAGAAGAAGCGTGGGTAGCAG
<i>GhMEKK12-RT-R</i>	TGCCACTAATCTCTAAGTCTAAGCC
<i>GhMEKK24-RT-F</i>	TTTCGTCTCGAAGGAACCGACG
<i>GhMEKK24-RT-R</i>	CCGAGGCAGAAGATCCGATGAC
<i>GhMEKK31-RT-F</i>	TTTCGTCTCGAAGGAACCGACG
<i>GhMEKK31-RT-R</i>	CCGAGGCAGAAGATCCGATGAC
<i>GhMEKK36-RT-F</i>	CGGATTCTCATCTGATGTGCCTGA
<i>GhMEKK36-RT-R</i>	CAATACGCTGCTGGGTGTCTCA
<i>GhMEKK40-RT-F</i>	ACGGTTGAGAAGGGTGAGAAGT
<i>GhMEKK40-RT-R</i>	GGATTCAATCAAGTTTCCGCCGC
<i>GhRAF4-RT-F</i>	CCCACCGAAGAGGCCGTAAAAT
<i>GhRAF4-RT-R</i>	CCAACATTCTCCGATGAGCTCCC
<i>GhRAF8-RT-F</i>	CTGGCAACAGGACCCAACTCAA
<i>GhRAF8-RT-R</i>	GGCGATCTTCCCCCTTATCTGC
<i>GhRAF21-RT-F</i>	GAACCGTGCTGTGCCATTGAAG
<i>GhRAF21-RT-R</i>	TCTGGTGTCATGCCCTCAGTCT
<i>GhRAF78-RT-F</i>	CTGCGAGCATCATTTCGGCAAG
<i>GhRAF78-RT-R</i>	CCATTGAGGCCCCCAAACTT
<i>GhRAF87-RT-F</i>	TCTTACGGCCAAAGTGGAAGCC
<i>GhRAF87-RT-R</i>	GACAGCTACAGGTGTTCCCTCGC
<i>GhUBI1-F</i>	CTGAATCTTCGCTTTCACGTTATC
<i>GhUBI1-R</i>	GGGATGCAAATCTTCGTGAAAAC

A



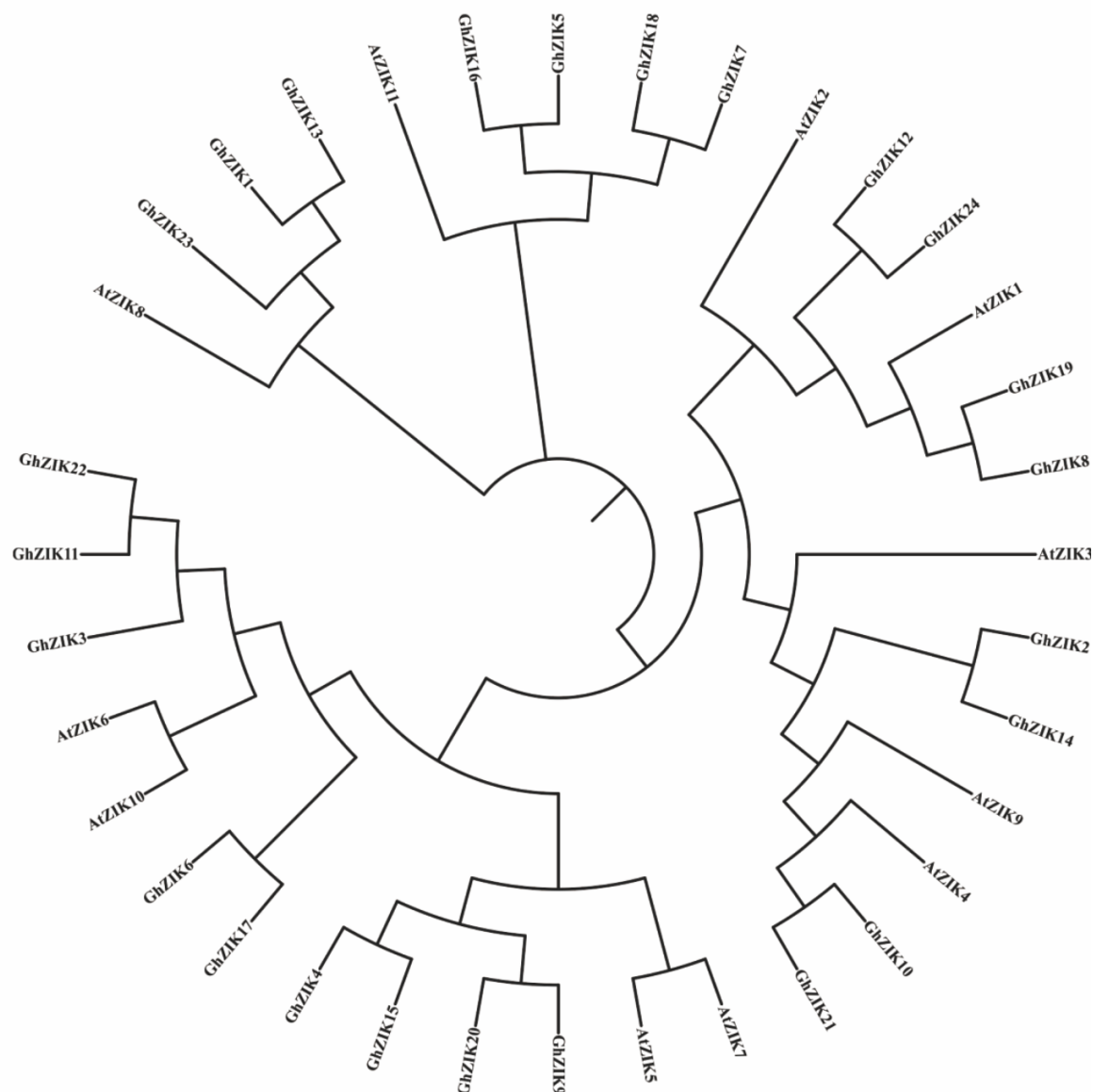
C

Figure S1. Phylogenetic relationship of GhMAPKKKs and AtMAPKKKs. (A) Phylogenetic relationship of GhRAFs and AtRAFs. (B) Phylogenetic relationship of GhRAFs and AtMEKKs. (C) Phylogenetic relationship of GhZIKs and AtZIKs. The unrooted phylogenetic tree was constructed using MEGA 6.0 by Neighbor-Joining method and the bootstrap test was performed with 1,000 iterations. Gh, upland cotton; At, Arabidopsis.

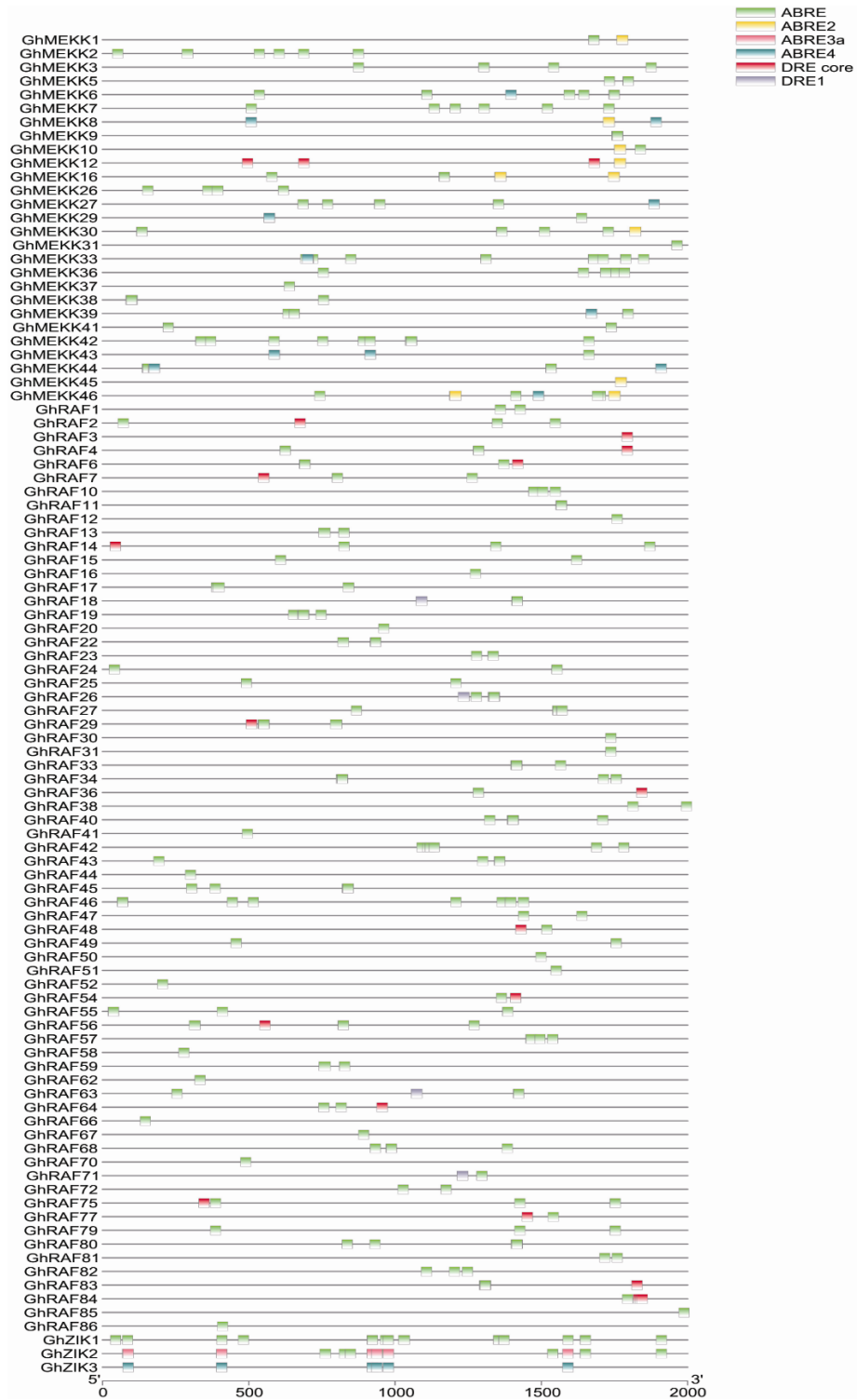


Figure S2. Analysis of *GhMAPKKK* promoters. The cis-elements existed in the promoter sequences were identified in cotton MAPKKK gene family. Each cis-element is indicated with a specific color.